

SEQUENCE LISTING

<110> Funahashi, Shin-ichi
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<120> NOVEL GENE ENCODING BRAIN-SPECIFIC MEMBRANE PROTEIN

<130> 06501-081001

<140> 09/831,846

<141> 2001-05-15

<150> PCT/JP99/06449

<151> 1999-11-18

<150> JP 10/331727

<151> 1998-11-20

<160> 7

<210> 1

<211> 3144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (466)..(2832)

<400> 1

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tcttcgatcc ggaaaatcct accggcatcc tctaggggag ggattattat tattatTTTT      180
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc      240
catggatata actgaataag cggctcaggg ctttccccgc gtggacgtcc gaggccacca      300
tctgacctga ttcgccggag ccgccggagg gtttagctcg agtctgtctc gggcggggaa      360
ggatgcgtgg ccgagccggg gagcccgggc gcccccgga gccggcctcg gtgccacca      420
gccgggggta gatgctgcct cgcccaggcg ctgagtgacc agacc atg gag acc ctg      477
                                         Met Glu Thr Leu
                                         1

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ctt ggt ggc ctg cta gcg ttt ggc atg gcg ttt gcc gtg gtc gac gcc      525
Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala
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tgc ccc aag tac tgt gtc tgc cag aat ctg tct gag tca ctg ggg acc      573
Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr
                25                30                35

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ctg tgc ccc tcc aag ggg ctg ctc ttt gta ccc cct gat att gac cgg      621
Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg
                40                45                50

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cgg aca gtg gag ctg cgc ctg ggc ggc aac ttc atc atc cac atc agc	669
Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser	
55 60 65	
cgc cag gac ttt gcc aac atg acg ggg ctg gtg gac ctg acc ctg tcc	717
Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser	
70 75 80	
agg aac acc atc agc cac atc cag ccc ttt tcc ttt ctg gac ctc gag	765
Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu	
85 90 95 100	
agc ctc cgc tcc ctg cat ctt gac agc aat cgg ctg cca agc ctt ggg	813
Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly	
105 110 115	
gag gac acc ctc cgg ggc ctg gtc aac ctg cag cac ctt atc gtg aac	861
Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn	
120 125 130	
aac aac cag ctg ggc ggc atc gca gat gag gct ttt gag gac ttc ctg	909
Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu	
135 140 145	
ctg aca ttg gag gat ctg gac ctc tcc tac aac aac ctc cat ggc ctg	957
Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu	
150 155 160	
ccg tgg gac tcc gtg cga cgc atg gtc aac ctc cac cag ctg agc ctg	1005
Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu	
165 170 175 180	
gac cac aac ctg ctg gat cac atc gcc gag ggc acc ttt gca gac ctg	1053
Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu	
185 190 195	
cag aaa ctg gcc cgc ctg gat ctc acc tcc aat cgg ctg cag aag ctg	1101
Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu	
200 205 210	
ccc cct gat ccc atc ttt gcc cgc tcc cag gct tcg gct ttg aca gcc	1149
Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala	
215 220 225	
aca ccc ttt gcc cca ccc ttg tcc ttt agt ttt ggg ggt aac cca ctt	1197
Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu	
230 235 240	
cac tgc aat tgt gag ctt ctc tgg ctg cgg agg ctc gag cgg gac gat	1245
His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp	
245 250 255 260	
gac ctg gaa acc tgt ggc tcc cca ggg ggc ctc aag ggt cgc tac ttc	1293
Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe	
265 270 275	
tgg cat gtg cgt gag gag gag ttt gtg tgc gag ccg cct ctc atc acc	1341

Trp	His	Val	Arg	Glu	Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Leu	Ile	Thr		
			280					285					290				
cag	cac	aca	cac	aag	ttg	ctg	gtt	ctg	gag	ggc	cag	gcg	gcc	aca	ctc		1389
Gln	His	Thr	His	Lys	Leu	Leu	Val	Leu	Glu	Gly	Gln	Ala	Ala	Thr	Leu		
		295					300					305					
aag	tgc	aaa	gcc	att	ggg	gac	ccc	agc	ccc	ctt	atc	cac	tgg	gta	gcc		1437
Lys	Cys	Lys	Ala	Ile	Gly	Asp	Pro	Ser	Pro	Leu	Ile	His	Trp	Val	Ala		
	310					315					320						
ccc	gat	gac	cgc	ctg	gta	ggg	aac	tcc	tca	agg	acc	gct	gtc	tat	gac		1485
Pro	Asp	Asp	Arg	Leu	Val	Gly	Asn	Ser	Ser	Arg	Thr	Ala	Val	Tyr	Asp		
325					330					335					340		
aat	ggc	acc	ctg	gac	atc	ttc	atc	acc	aca	tct	cag	gac	agt	ggg	gcc		1533
Asn	Gly	Thr	Leu	Asp	Ile	Phe	Ile	Thr	Thr	Ser	Gln	Asp	Ser	Gly	Ala		
			345					350						355			
ttc	acc	tgc	att	gct	gcc	aat	gct	gcc	gga	gag	gcc	acg	gcc	atg	gtg		1581
Phe	Thr	Cys	Ile	Ala	Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Met	Val		
			360					365					370				
gag	gtc	tcc	atc	gtc	cag	ctg	cca	cac	ctc	agc	aac	agc	acc	agc	cgc		1629
Glu	Val	Ser	Ile	Val	Gln	Leu	Pro	His	Leu	Ser	Asn	Ser	Thr	Ser	Arg		
		375					380					385					
act	gca	ccc	ccc	aag	tcc	cgc	ctc	tca	gac	atc	act	ggc	tcc	agc	aag		1677
Thr	Ala	Pro	Pro	Lys	Ser	Arg	Leu	Ser	Asp	Ile	Thr	Gly	Ser	Ser	Lys		
	390					395					400						
acc	agc	cgg	gga	ggg	gga	ggc	agt	ggg	ggc	gga	gag	cct	ccc	aaa	agc		1725
Thr	Ser	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Ser		
405					410					415					420		
ccc	ccg	gaa	cgg	gct	gtg	ctt	gtg	tct	gaa	gtg	acc	acc	acc	tcg	gcc		1773
Pro	Pro	Glu	Arg	Ala	Val	Leu	Val	Ser	Glu	Val	Thr	Thr	Thr	Ser	Ala		
				425					430					435			
ctg	gtc	aag	tgg	tct	gtc	agc	aag	tca	gca	ccc	cgg	gtg	aag	atg	tac		1821
Leu	Val	Lys	Trp	Ser	Val	Ser	Lys	Ser	Ala	Pro	Arg	Val	Lys	Met	Tyr		
			440					445					450				
cag	ctg	cag	tac	aac	tgc	tct	gac	gat	gag	gta	ctg	att	tac	agg	atg		1869
Gln	Leu	Gln	Tyr	Asn	Cys	Ser	Asp	Asp	Glu	Val	Leu	Ile	Tyr	Arg	Met		
		455					460						465				
atc	cca	gcc	tcc	aac	aag	gcc	ttc	gtg	gtc	aac	aac	ctg	gtg	tca	ggg		1917
Ile	Pro	Ala	Ser	Asn	Lys	Ala	Phe	Val	Val	Asn	Asn	Leu	Val	Ser	Gly		
	470					475					480						
act	ggc	tac	gac	ttg	tgt	gtg	ctg	gcc	atg	tgg	gat	gac	aca	gcc	acg		1965
Thr	Gly	Tyr	Asp	Leu	Cys	Val	Leu	Ala	Met	Trp	Asp	Asp	Thr	Ala	Thr		
485					490					495					500		
aca	ctc	acg	gcc	acc	aac	atc	gtg	ggc	tgc	gcc	cag	ttc	ttc	acc	aag		2013
Thr	Leu	Thr	Ala	Thr	Asn	Ile	Val	Gly	Cys	Ala	Gln	Phe	Phe	Thr	Lys		

505 510 515

gct gac tac ccg cag tgc cag tcc atg cac agc cag att ctg ggc ggc 2061																				
Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly																				
520 525 530																				
acc atg atc ctg gtc atc ggg ggc atc atc gtg gcc acg ctg ctg gtc 2109																				
Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val																				
535 540 545																				
ttc atc gtc atc ctc atg gtg cgc tac aag gtc tgc aac cac gag gcc 2157																				
Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala																				
550 555 560																				
ccc agc aag atg gca gcg gcc gtg agc aat gtg tac tcg cag acc aac 2205																				
Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn																				
565 570 575 580																				
ggc gcc cag cca ccg cct cca agc agc gca cca gcc ggg gcc ccg ccg 2253																				
Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro																				
585 590 595																				
cag ggc ccg ccg aag gtg gtg gtg cgc aac gag ctc ctg gac ttc acc 2301																				
Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr																				
600 605 610																				
gcc agc ctg gcc cgc gcc agt gac tcc tct tcc tcc agc tcc ctg ggc 2349																				
Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly																				
615 620 625																				
agt ggg gag gct gcg ggg ctg gga cgg gcc ccc tgg agg atc cca ccc 2397																				
Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro																				
630 635 640																				
tcc gcc ccg cgc ccc aag ccc agc ctt gac cgc ctg atg ggg gcc ttc 2445																				
Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe																				
645 650 655 660																				
gcc tcc ctg gac ctc aag agt cag aga aag gag gag ctg ctg gac tcc 2493																				
Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser																				
665 670 675																				
agg act cca gcc ggg aga ggg gct ggg acg tcg gcc cgg ggc cac cac 2541																				
Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His																				
680 685 690																				
tcg gac cga gag cca ctg ctg ggg ccc cct gcg gcc cgg gcc agg agc 2589																				
Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser																				
695 700 705																				
ctg ctc ccc ttg ccg ttg gag ggc aag gcc aaa cgc agc cac tcc ttc 2637																				
Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe																				
710 715 720																				
gac atg ggg gac ttt gct gct gcg gcg gcg gga ggg gtc gtg ccg ggc 2685																				
Asp Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly																				
725 730 735 740																				

ggc tac agt cct cct cgg aag gtc tcg aac atc tgg acg aag cgc agc 2733
 Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser
 745 750 755

ctc tct gtc aac ggc atg ctc ttg ccc ttt gag gag agt gac ctg gtg 2781
 Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val
 760 765 770

ggg gcc cgg ggg act ttt ggc agc tcc gaa tgg gtg atg gag agc acg 2829
 Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr
 775 780 785

gtc taggtggggg tgggcatgct ccccttctcg tgcgcagggt gggagaaggg 2882
 Val

gaaagaatct cactggcaag tgtttgtgga gtttccatgg tgatgtttac atccagggac 2942
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<211> 789

<212> PRT

<213> Homo sapiens

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 20 25 30
 Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro
 35 40 45
 Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile
 50 55 60
 Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp
 65 70 75 80
 Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe
 85 90 95
 Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu
 100 105 110
 Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His
 115 120 125
 Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe
 130 135 140
 Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn
 145 150 155 160
 Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His
 165 170 175
 Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr
 180 185 190
 Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg
 195 200 205
 Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser
 210 215 220

	675		680		685												
Arg	Gly	His	His	Ser	Asp	Arg	Glu	Pro	Leu	Leu	Gly	Pro	Pro	Ala	Ala		
	690					695					700						
Arg	Ala	Arg	Ser	Leu	Leu	Pro	Leu	Pro	Leu	Glu	Gly	Lys	Ala	Lys	Arg		
705					710					715					720		
Ser	His	Ser	Phe	Asp	Met	Gly	Asp	Phe	Ala	Ala	Ala	Ala	Ala	Gly	Gly		
				725					730						735		
Val	Val	Pro	Gly	Tyr	Ser	Pro	Pro	Arg	Lys	Val	Ser	Asn	Ile	Trp			
			740					745					750				
Thr	Lys	Arg	Ser	Leu	Ser	Val	Asn	Gly	Met	Leu	Leu	Pro	Phe	Glu	Glu		
		755					760						765				
Ser	Asp	Leu	Val	Gly	Ala	Arg	Gly	Thr	Phe	Gly	Ser	Ser	Glu	Trp	Val		
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Met	Glu	Ser	Thr	Val													
785																	

<210> 3

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an artificially synthesized primer sequence.

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<210> 4

<211> 16

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an artificially synthesized adapter sequence.

<400> 4

tcgaccacg cgccg

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<210> 5

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an artificially synthesized adapter sequence.

<400> 5

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12

<210> 6

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an artificially synthesized primer sequence.

<400> 6

caggggtggga gaaggggaaa gaatc

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<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an artificially synthesized primer sequence.

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25

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